GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 22:06:02 ; Search time 2719.38 Seconds
(without alignments)
12110.308 Million cell updates/sec

Title: US-09-904-568-3
Perfect score: 1355
Sequence: 1 gggcaggcagttgaggtgga.....gtgtttcaggcagggcccgg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 6312

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14.2	1.0	19	9	AI702520	AI702520 tz67g05.x
	2	14	1.0	20	28	AZ345513	AZ345513 1M0080J04
	3	13.6	1.0	20	28	AZ764505	AZ764505 1M0560M06
	4	13.4	1.0	19	9	AA928040	AA928040 oi58g09.s
	5	13.4	1.0	19	28	AZ465954	AZ465954 1M0276E16
c	6	13.4	1.0	19	28	AZ486389	AZ486389 1M0314E21
	7	13.4	1.0	20	9	AL587572	AL587572 AL587572
c	8	13.4	1.0	20	28	AZ821905	AZ821905 2M0094D20
c	9	13.2	1.0	19	28	AZ429998	AZ429998 1M0214F16
	10	13.2	1.0	19	28	AZ456215	AZ456215 1M0258K21
	11	13	1.0	18	12	BM658677	BM658677 LZV602768
c	12	13	1.0	19	28	AZ360314	AZ360314 1M0103G03
	13	13	1.0	19	28	AZ513919	AZ513919 1M0360E13
	14	13	1.0	19	28	AZ645841	AZ645841 1M0511G04
c	15	12.8	0.9	18	9	AL048754	AL048754 DKFZp566L
	16	12.8	0.9	19	28	AZ819620	AZ819620 2M0091A23
c	17	12.8	0.9	19	28	AZ995149	AZ995149 2M0280D22
c	18	12.8	0.9	20	2	HSM002936	Al038460 Homo sapi
c	19	12.8	0.9	20	28	AZ430735	AZ430735 1M0215A22
	20	12.8	0.9	20	28	AZ468517	AZ468517 1M0281N01
c	21	12.8	0.9	20	28	AZ628029	AZ628029 1M0476F17
c	22	12.8	0.9	20	28	AZ665192	AZ665192 1M0546C04
	23	12.8	0.9	20	29	TA339H11Q	AL492631 T. brucei
c	24	12.6	0.9	19	9	AI584018	AI584018 ts12e10.x
c	25	12.6	0.9	19	28	AZ394490	AZ394490 1M0158O05
c	26	12.6	0.9	19	28	AZ422163	AZ422163 1M0200B22
c	27	12.6	0.9	19	28	AZ427411	AZ427411 1M0209A22
c	28	12.6	0.9	19	28	AZ759607	AZ759607 1M0552I23
c	29	12.6	0.9	19	28	AZ775624	AZ775624 2M0008E01
	30	12.6	0.9	19	28	AZ825396	AZ825396 2M0100N04
	31	12.6	0.9	20	14	C20903	C20903 HUMGS000498
c	32	12.6	0.9	20	28	AZ386669	AZ386669 1M0145G15
c	33	12.6	0.9	20	28	AZ426873	AZ426873 1M0208L05
	34	12.6	0.9	20	28	AZ469472	AZ469472 1M0283A06
	35	12.6	0.9	20	28	AZ486787	AZ486787 1M0315D23
c	36	12.6	0.9	20	28	AZ633741	AZ633741 1M0489G12
c	37	12.6	0.9	20	28	AZ823352	AZ823352 2M0097A22
c	38	12.6	0.9	20	28	AZ830285	AZ830285 2M0109N22
	39	12.4	0.9	16	13	BQ590207	BQ590207 E012843-0
	40	12.4	0.9	19	28	AZ308423	AZ308423 1M0011E21
c	41	12.4	0.9	19	28	AZ474038	AZ474038 1M0290G15
	42	12.4	0.9	19	28	AZ585820	AZ585820 1M0391I15
c	43	12.4	0.9	19	28	AZ650252	AZ650252 1M0520N17
	44	12.4	0.9	20	9	AL587727	AL587727 AL587727
	45	12.4	0.9	20	28	AZ345856	AZ345856 1M0080G17

ALIGNMENTS

RESULT 1
AI702520/c
LOCUS AI702520 19 bp mRNA linear EST 16-DEC-1999
DEFINITION tz67g05.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2293688 3' similar to WP:D1007.7 CE09042 RNA-BINDING PROTEIN ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI702520
VERSION AI702520.1 GI:4990420
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

```
            Insert Length: 2437   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:2293688"
                        /tissue_type="adenocarcinoma"
                        /lab_host="DH10B"
                        /clone_lib="NCI_CGAP_Pan1"
                        /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                        Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                        Average insert size 1.72 kb. Life Technologies catalog #:
                        11548-013"
BASE COUNT          2 a      2 c     15 g      0 t
ORIGIN

  Query Match             1.0%;  Score 14.2;  DB 9;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 5e+07;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        184 TTCCCCGCCGCCCACCCGG 202
              |||||| || ||| |||||
Db         19 TTCCCCCCCCCCCCCCCGG 1


RESULT 2
AZ345513
LOCUS       AZ345513                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080J04 F, genomic survey sequence.
ACCESSION   AZ345513
VERSION     AZ345513.1  GI:10424750
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: J  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC1M0080J04"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /note="Vector: PWD42nv; Purified genomic DNA from M.
                        musculus C57BL/6J (male) was obtained  from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high  molar excess. The
                        adaptored DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adaptored mouse DNA was annealed to
                        adaptored vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."
BASE COUNT          3 a     13 c      0 g      4 t
ORIGIN

  Query Match             1.0%;  Score 14;  DB 28;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+07;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1208 ACCTCCCCTTCCCT 1221
              ||||||||||||||
Db          1 ACCTCCCCTTCCCT 14


RESULT 3
AZ764505
LOCUS       AZ764505                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560M06 R, genomic survey sequence.
ACCESSION   AZ764505
VERSION     AZ764505.1  GI:12879537
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: M  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC1M0560M06"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /note="Vector: PWD42nv; Purified genomic DNA from M.
```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 15 c 5 g 0 t
ORIGIN

Query Match 1.0%; Score 13.6; DB 28; Length 20;
Best Local Similarity 80.0%; Pred. No. 7e+07;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 186 CCCCGCCGCCCACCCGGACG 205
|||| || ||| ||||| ||
Db 1 CCCCCCCCCCCGCCCGGGCG 20

RESULT 4
AA928040
LOCUS AA928040 19 bp mRNA linear EST 22-APR-1998
DEFINITION oi58g09.s1 NCI_CGAP_HN4 Homo sapiens cDNA clone IMAGE:1486912 3' similar to TR:O04216 O04216 EXTENSIN ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION AA928040
VERSION AA928040.1 GI:3077196
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John Ensley, M.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1486912"
/tissue_type="squamous cell carcinoma"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI_CGAP_HN4"
/note="Organ: pharynx; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence: 5' GAATTCGGCACGAG 3' 3' adaptor sequence: 5' (GA)10ACTAGTCTCGAGTTTTTTTTTTTTTTTT 3'"

BASE COUNT 2 a 1 c 11 g 5 t
ORIGIN

Query Match 1.0%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 659 TGGTCGGGGACTTGG 673
|||| ||||||||||
Db 5 TGGTGGGGGACTTGG 19

RESULT 5
AZ465954
LOCUS AZ465954 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0276E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0276E16 F, genomic survey sequence.
ACCESSION AZ465954
VERSION AZ465954.1 GI:10624079
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: E column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0276E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 0 a 5 c 0 g 14 t
ORIGIN

Query Match 1.0%; Score 13.4; DB 28; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1142 CCTTTTTTTCTTTTT 1156
||||||||| |||||
Db 4 CCTTTTTTTTTTTTT 18

RESULT 6
AZ486389/c
LOCUS AZ486389 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0314E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0314E21 F, genomic survey sequence.
ACCESSION AZ486389
VERSION AZ486389.1 GI:10653117
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0314 row: E column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0314E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 7 a 2 c 7 g 3 t
ORIGIN

Query Match 1.0%; Score 13.4; DB 28; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1062 CCTTCCCATCAGGCA 1076
| ||||||||||||||
Db 18 CTTTCCCATCAGGCA 4

RESULT 7
AL587572
LOCUS AL587572 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone ROS059B11, mRNA sequence.
ACCESSION AL587572
VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1. .20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"
BASE COUNT 0 a 0 c 2 g 18 t
ORIGIN

Query Match 1.0%; Score 13.4; DB 9; Length 20;
Best Local Similarity 93.3%; Pred. No. 7.8e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1144 TTTTTTTCTTTTTGG 1158
||||||| |||||||
Db 6 TTTTTTTTTTTTTGG 20

RESULT 8
AZ821905/c
LOCUS AZ821905 20 bp DNA linear GSS 20-FEB-2001

```
DEFINITION  2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0094D20 R, genomic survey sequence.
ACCESSION   AZ821905
VERSION     AZ821905.1  GI:12991813
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0094  row: D  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0094D20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       18 a      2 c      0 g      0 t
ORIGIN

  Query Match             1.0%;  Score 13.4;  DB 28;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 7.8e+07;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGG 1158
              ||||||| |||||||
Db         15 TTTTTTTTTTTTTGG 1


RESULT 9
AZ429998/c
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LOCUS       AZ429998                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0214F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0214F16 F, genomic survey sequence.
ACCESSION   AZ429998
VERSION     AZ429998.1  GI:10554011
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0214  row: F  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0214F16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        5 a      3 c      9 g      2 t
ORIGIN

  Query Match             1.0%;  Score 13.2;  DB 28;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+07;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGCATC 648
              ||||| |  |||||||||
Db         18 CTCCATGGCCTCTGCATC 1


RESULT 10
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AZ456215
LOCUS       AZ456215                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0258K21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0258K21 R, genomic survey sequence.
ACCESSION   AZ456215
VERSION     AZ456215.1  GI:10614340
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0258  row: K  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0258K21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        4 a      3 c      3 g      9 t
ORIGIN

  Query Match             1.0%;  Score 13.2;  DB 28;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+07;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1173 AAACATGTTTCTATAGGT 1190
              | || ||||| |||||||
Db          2 ACACCTGTTTTTATAGGT 19
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RESULT 11
BM658677
LOCUS       BM658677                 18 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658677
VERSION     BM658677.1  GI:18958948
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."
BASE COUNT        0 a      1 c      0 g     17 t
ORIGIN

  Query Match             1.0%;  Score 13;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+07;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTT 1156
              |||||||||||||
Db          2 TTTTTTTCTTTTT 14
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RESULT 12
AZ360314/c
LOCUS       AZ360314                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION   AZ360314
VERSION     AZ360314.1  GI:10474014
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
```

```
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: G  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0103G03"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       17 a      0 c      2 g      0 t
ORIGIN

  Query Match             1.0%;  Score 13;  DB 28;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.6e+07;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTT 1156
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Db         16 TTTTTTTCTTTTT 4


RESULT 13
AZ513919
LOCUS       AZ513919                19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION   AZ513919
VERSION     AZ513919.1  GI:10695235
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0360  row: E  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0360E13"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant; F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        0 a      1 c      0 g     18 t
ORIGIN

  Query Match             1.0%;  Score 13;  DB 28;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.6e+07;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTT 1156
              |||||||||||||
Db          5 TTTTTTTCTTTTT 17


RESULT 14
AZ645841
LOCUS       AZ645841                19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0511G04 R, genomic survey sequence.
ACCESSION   AZ645841
VERSION     AZ645841.1  GI:11775726
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 0 g 18 t
ORIGIN

Query Match 1.0%; Score 13; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e+07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1144 TTTTTTCTTTTT 1156
              ||||||||||||
Db          2 TTTTTTCTTTTT 14
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RESULT 15
AL048754/c
LOCUS AL048754 18 bp mRNA linear EST 30-APR-1999
DEFINITION DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L173, mRNA sequence.
ACCESSION AL048754
VERSION AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished
COMMENT Contact: Koehrer K
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

BASE COUNT 16 a 1 c 0 g 1 t
ORIGIN

Query Match 0.9%; Score 12.8; DB 9; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.1e+08;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1144 TTTTTTCTTTTTGGA 1159
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Db         16 TTTTTTTTTTTTTGA 1
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Search completed: September 8, 2003, 02:28:52
Job time : 2723.38 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 18:52:18 ; Search time 362.069 Seconds
(without alignments)
8607.385 Million cell updates/sec

Title: US-09-904-568-3
Perfect score: 1355
Sequence: 1 gggcaggcagttgaggtgga.....gtgtttcaggcagggcccgg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1537136 seqs, 1149988732 residues

Total number of hits satisfying chosen parameters: 277732

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.4	1.2	18	11	US-09-876-235-29	Sequence 29, Appl
c	2	16	1.2	17	12	US-09-792-818-388	Sequence 388, App
c	3	16	1.2	17	12	US-09-792-818-389	Sequence 389, App
c	4	15.8	1.2	20	10	US-09-791-243-25	Sequence 25, Appl
c	5	15.8	1.2	20	11	US-09-842-758-79	Sequence 79, Appl
c	6	15.8	1.2	20	12	US-10-006-972A-87	Sequence 87, Appl
c	7	15.8	1.2	20	14	US-10-005-715-2	Sequence 2, Appli
c	8	15.4	1.1	18	9	US-09-813-289-4	Sequence 4, Appli
c	9	15.4	1.1	18	12	US-09-809-920-19	Sequence 19, Appl
c	10	15.4	1.1	20	12	US-10-024-369-81	Sequence 81, Appl
c	11	15.2	1.1	20	10	US-09-780-172-69	Sequence 69, Appl
c	12	15.2	1.1	20	11	US-09-989-420-23	Sequence 23, Appl
	13	15.2	1.1	20	11	US-09-948-002-55	Sequence 55, Appl
	14	15.2	1.1	20	11	US-09-954-556-94	Sequence 94, Appl
	15	15.2	1.1	20	14	US-10-116-949-33	Sequence 33, Appl
	16	15.2	1.1	20	14	US-10-116-949-43	Sequence 43, Appl
	17	15.2	1.1	20	14	US-10-067-443-16	Sequence 16, Appl
	18	15.2	1.1	20	14	US-10-271-887-168	Sequence 168, App
c	19	15	1.1	17	12	US-09-792-818-387	Sequence 387, App
c	20	15	1.1	17	12	US-09-792-818-390	Sequence 390, App
c	21	14.8	1.1	19	10	US-09-969-373-1795	Sequence 1795, Ap
c	22	14.8	1.1	20	11	US-09-539-382-23	Sequence 23, Appl
c	23	14.8	1.1	20	11	US-09-919-197-42	Sequence 42, Appl
c	24	14.8	1.1	20	14	US-10-067-790-23	Sequence 23, Appl
c	25	14.8	1.1	20	14	US-10-067-892-23	Sequence 23, Appl
c	26	14.8	1.1	20	14	US-10-067-893-23	Sequence 23, Appl
c	27	14.8	1.1	20	14	US-10-263-872-35	Sequence 35, Appl
	28	14.4	1.1	17	10	US-09-864-785-1485	Sequence 1485, Ap
	29	14.4	1.1	17	10	US-09-864-785-2738	Sequence 2738, Ap
c	30	14.4	1.1	18	10	US-09-880-732-49	Sequence 49, Appl
c	31	14.4	1.1	18	11	US-09-967-237-113	Sequence 113, App
c	32	14.4	1.1	19	10	US-09-880-732-50	Sequence 50, Appl
c	33	14.4	1.1	20	8	US-08-983-605-364	Sequence 364, App
c	34	14.4	1.1	20	9	US-09-752-983-48	Sequence 48, Appl
c	35	14.4	1.1	20	10	US-09-877-935-7	Sequence 7, Appli
c	36	14.4	1.1	20	11	US-09-863-049A-17	Sequence 17, Appl
c	37	14.4	1.1	20	11	US-09-920-033-109	Sequence 109, App
	38	14.2	1.0	19	11	US-09-880-313A-120	Sequence 120, App
c	39	14.2	1.0	20	9	US-09-758-881-16	Sequence 16, Appl
c	40	14.2	1.0	20	9	US-09-758-881-68	Sequence 68, Appl
c	41	14.2	1.0	20	9	US-09-992-901-4	Sequence 4, Appli
	42	14.2	1.0	20	11	US-09-774-809-123	Sequence 123, App
c	43	14.2	1.0	20	11	US-09-915-485-52	Sequence 52, Appl
c	44	14.2	1.0	20	11	US-09-953-047-85	Sequence 85, Appl
c	45	14.2	1.0	20	11	US-09-972-607-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-876-235-29
; Sequence 29, Application US/09876235
; Publication No. US20030022236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/876,235
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-235-29

Query Match 1.2%; Score 16.4; DB 11; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        679 GTGGTATTTGGGAGCCAG 696
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Db          1 GTGGTATTTGTGAGCCAG 18
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RESULT 2

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US-09-792-818-388/c
; Sequence 388, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  Von Carlowitz, Ira
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Hamblin, Paul
;  APPLICANT:  Ellis, Jonathan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inser
;  TITLE OF INVENTION:  (GRID) Gene
;  FILE REFERENCE: MBHB00-901-A (400/013)
;  CURRENT APPLICATION NUMBER: US/09/792,818
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS: 2304
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 388
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-792-818-388

  Query Match             1.2%;  Score 16;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTGC 314
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Db         17 CTGCTGTGGGGGCTGC 2


RESULT 3
US-09-792-818-389/c
; Sequence 389, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  Von Carlowitz, Ira
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Hamblin, Paul
;  APPLICANT:  Ellis, Jonathan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inser
;  TITLE OF INVENTION:  (GRID) Gene
;  FILE REFERENCE: MBHB00-901-A (400/013)
;  CURRENT APPLICATION NUMBER: US/09/792,818
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS: 2304
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-792-818-389

  Query Match             1.2%;  Score 16;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTGC 314
              ||||||||||||||||
Db         16 CTGCTGTGGGGGCTGC 1


RESULT 4
US-09-791-243-25/c
; Sequence 25, Application US/09791243
; Patent No. US20020147164A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Robert Rothlein
;  APPLICANT:  Takashi Kei Kishimoto
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOHESIN-1 EXPRESSION
;  FILE REFERENCE: RTS-0095
;  CURRENT APPLICATION NUMBER: US/09/791,243
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-243-25

  Query Match             1.2%;  Score 15.8;  DB 10;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.1e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              |||||||||||||||  ||
Db         20 ACCTGCCGGAGGAGCTCCT 2


RESULT 5
US-09-842-758-79/c
; Sequence 79, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine A. M.
;  APPLICANT:  Fernandes, Elma R
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Edward, Szekeres S
;  APPLICANT:  Alsobrook II, John P
;  TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 15966-783
;  CURRENT APPLICATION NUMBER: US/09/842,758
;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: 60/200,158
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: 60/200,613
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 60/200,780
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 60/201,006
;  PRIOR FILING DATE: 2000-05-01
;  PRIOR APPLICATION NUMBER: 60/201,007
;  PRIOR FILING DATE: 2000-05-01
;  PRIOR APPLICATION NUMBER: 60/201,236
;  PRIOR FILING DATE: 2000-05-01
;  PRIOR APPLICATION NUMBER: 60/201,238
;  PRIOR FILING DATE: 2000-05-01
;  PRIOR APPLICATION NUMBER: 60/201,186
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 60/201,474
;  PRIOR FILING DATE: 2000-05-03
;  PRIOR APPLICATION NUMBER: 60/201,508
;  PRIOR FILING DATE: 2000-05-03
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;  PRIOR APPLICATION NUMBER: 60/220,591
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: 60/232,678
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: 60/263,217
;  PRIOR FILING DATE: 2001-01-22
;  PRIOR APPLICATION NUMBER: 60/265,160
;  PRIOR FILING DATE: 2001-01-30
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Ag743 Forward
;   OTHER INFORMATION: Primer
US-09-842-758-79

  Query Match             1.2%;  Score 15.8;  DB 11;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.1e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        641 TCTGCATCCCCCAAGACCT 659
              ||||||||| |||||||  |
Db         19 TCTGCATCCACCAAGACAT 1


RESULT 6
US-10-006-972A-87/c
; Sequence 87, Application US/10006972A
; Publication No. US20030139359A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 3 EXPRESSION
;  FILE REFERENCE: RTS-0335
;  CURRENT APPLICATION NUMBER: US/10/006,972A
;  CURRENT FILING DATE:  2001-12-04
;  NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 87
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-972A-87

  Query Match             1.2%;  Score 15.8;  DB 12;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.1e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGCATCC 649
              ||||||||| ||| |||||
Db         19 CTCCAGGAGTTCTCCATCC 1


RESULT 7
US-10-005-715-2/c
; Sequence 2, Application US/10005715
; Publication No. US20030023058A1
; GENERAL INFORMATION:
;  APPLICANT: University of No. US20030023058A1th Carolina at Chapel Hill
;  APPLICANT:  Weston, Brent W.
;  APPLICANT:  Hiller, Kara M.
;  TITLE OF INVENTION: ANTISENSE HUMAN FUCOSYLTRANSFERASE SEQUENCES AND METHODS OF USE T
;  FILE REFERENCE: 5470-259CT
;  CURRENT APPLICATION NUMBER: US/10/005,715
;  CURRENT FILING DATE:  2002-03-21
;  PRIOR APPLICATION NUMBER: US 60/131,068
;  PRIOR FILING DATE: 1999-04-26
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-005-715-2

  Query Match             1.2%;  Score 15.8;  DB 14;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.1e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1322 CTTTTGTAGATCTTGTGTT 1340
              |||||||||||||||  |||
Db         19 CTTTTGTAGATCTTCAGTT 1


RESULT 8
US-09-813-289-4/c
; Sequence 4, Application US/09813289
; Patent No. US20020061571A1
; GENERAL INFORMATION:
;  APPLICANT: Mahadevan, M.S.
;  APPLICANT:  Tiscornia, G
;  TITLE OF INVENTION: No. US20020061571A1el isoform of myotonic dystrophy associated
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE: 800.027US1
;  CURRENT APPLICATION NUMBER: US/09/813,289
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/190,590
;  PRIOR FILING DATE: 2000-03-20
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-813-289-4

  Query Match             1.1%;  Score 15.4;  DB 9;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 6.4e+05;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        578 AGGCCCTCCGTCTGCCC 594
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Db         17 AGGCCCTCCATCTGCCC 1


RESULT 9
US-09-809-920-19/c
; Sequence 19, Application US/09809920
; Publication No. US20030139584A1
;   GENERAL INFORMATION:
;        APPLICANT: Sato, Takaaki
;        TITLE OF INVENTION: TREX,  A NOVEL GENE OF TRAF-INTERACTING
;                            EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
;                            THEREOF
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Cooper & Dunham LLP
;             STREET: 1185 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/809,920
;             FILING DATE: 16-Mar-2001
;             CLASSIFICATION: <Unknown>
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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/156,191
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: White, John P.
;            REGISTRATION NUMBER: 28,678
;            REFERENCE/DOCKET NUMBER: 0575/51902
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 278-0400
;            TELEFAX: (212) 391-0525
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-809-920-19

  Query Match             1.1%;  Score 15.4;  DB 12;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 6.4e+05;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTCT 643
              ||||| ||||||||||
Db         18 CCAGCTGCAGGAGCTCT 2


RESULT 10
US-10-024-369-81/c
; Sequence 81, Application US/10024369
; Publication No. US20030134809A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander H. Borchers
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
;  FILE REFERENCE: RTS-0353
;  CURRENT APPLICATION NUMBER: US/10/024,369
;  CURRENT FILING DATE:  2001-12-17
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 81
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-81

  Query Match             1.1%;  Score 15.4;  DB 12;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 6.8e+05;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        785 CCACCAGTGCCCTGGCT 801
              ||||||||||||||| |
Db         17 CCACCAGTGCCCTGGAT 1


RESULT 11
US-09-780-172-69/c
; Sequence 69, Application US/09780172
; Patent No. US20020147163A1
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
;  FILE REFERENCE: RTS-0159
;  CURRENT APPLICATION NUMBER: US/09/780,172
;  CURRENT FILING DATE:  2001-02-08
;  NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 69
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-172-69

  Query Match             1.1%;  Score 15.2;  DB 10;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 7.8e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1070 TCAGGCAGGCTCTTCAGTGA 1089
              || ||||||||| ||||||
Db         20 TCTGGCAGGCTCACCAGTGA 1


RESULT 12
US-09-989-420-23/c
; Sequence 23, Application US/09989420
; Publication No. US20030013671A1
; GENERAL INFORMATION:
;  APPLICANT: MINENO, Junichi et al.
;  TITLE OF INVENTION: Genomic DNA library
;  FILE REFERENCE: 1422-0506P
;  CURRENT APPLICATION NUMBER: US/09/989,420
;  CURRENT FILING DATE:  2001-11-21
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: a sequence of a primer for
;   OTHER INFORMATION: cyclin E1 gene
US-09-989-420-23

  Query Match             1.1%;  Score 15.2;  DB 11;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 7.8e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1238 TGCTGGACGTGGCCATGTGA 1257
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Db         20 TGCGGGACGTGGACATCTGA 1


RESULT.13
US-09-948-002-55
; Sequence 55, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan F. Murray
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
;  TITLE OF INVENTION:  FACTOR BETA   EXPRESSION
;  FILE REFERENCE: ISPH-0607
;  CURRENT APPLICATION NUMBER: US/09/948,002
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: 09/661,753
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: 60/154,546
;  PRIOR FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-55

  Query Match             1.1%;  Score 15.2;  DB 11;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 7.8e+05;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        621 CAGGGACCAGCTCCAGGAGC 640
              | |||||||| | |||||||
Db          1 CCGGGACCAGATGCAGGAGC 20
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RESULT 14
US-09-954-556-94
; Sequence 94, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-94

Query Match 1.1%; Score 15.2; DB 11; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        856 TACCGCTTTGAGGTCCCCAC 875
              | || || ||||||||||||
Db          1 TGCCTCTGTGAGGTCCCCAC 20
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RESULT 15
US-10-116-949-33
; Sequence 33, Application US/10116949
; Publication No. US20030044911A1
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/10/116,949
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-33

Query Match 1.1%; Score 15.2; DB 14; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        335 CTGGTGATAGTCACAGTGGC 354
              |||||||| ||||||| ||
Db          1 CTGGTGATGGTCACAGGAGC 20
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Search completed: September 7, 2003, 22:23:28
Job time : 363.069 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 16:21:56 ; Search time 96.5886 Seconds
(without alignments)
6191.975 Million cell updates/sec

Title: US-09-904-568-3
Perfect score: 1355
Sequence: 1 gggcaggcagttgaggtgga.....gtgtttcaggcagggcccgg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 310906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.4	1.2	18	3	US-09-244-794A-29	Sequence 29, Appl
	2	16.4	1.2	18	3	US-09-007-005-29	Sequence 29, Appl
	3	16.4	1.2	18	3	US-09-247-190-29	Sequence 29, Appl
	4	16.4	1.2	18	3	US-09-244-796-29	Sequence 29, Appl
	5	16.4	1.2	18	4	US-09-238-710-29	Sequence 29, Appl
	6	15.8	1.2	20	3	US-09-136-959A-6	Sequence 6, Appli
c	7	15.8	1.2	20	4	US-09-556-031-2	Sequence 2, Appli
c	8	15.8	1.2	20	4	US-09-702-246-25	Sequence 25, Appl
	9	15.8	1.2	20	4	US-09-322-624-19	Sequence 19, Appl
c	10	15.4	1.1	20	4	US-09-422-978-11451	Sequence 11451, A
c	11	15.2	1.1	20	1	US-07-977-284A-89	Sequence 89, Appl
c	12	15.2	1.1	20	1	US-08-410-540-8	Sequence 8, Appli
c	13	15.2	1.1	20	2	US-08-256-426B-89	Sequence 89, Appl
	14	15.2	1.1	20	4	US-09-661-753-55	Sequence 55, Appl
	15	15.2	1.1	20	4	US-09-470-443-33	Sequence 33, Appl
	16	15.2	1.1	20	4	US-09-470-443-43	Sequence 43, Appl
	17	15.2	1.1	20	4	US-09-659-845A-168	Sequence 168, App
c	18	15.2	1.1	20	4	US-09-198-452A-1582	Sequence 1582, Ap
c	19	15.2	1.1	20	4	US-09-198-452A-3952	Sequence 3952, Ap
	20	15	1.1	15	4	US-09-081-646-727	Sequence 727, App
c	21	14.8	1.1	18	2	US-08-585-684B-2539	Sequence 2539, Ap
c	22	14.8	1.1	18	3	US-09-038-073-2539	Sequence 2539, Ap
	23	14.8	1.1	19	1	US-08-630-592-14	Sequence 14, Appl
	24	14.8	1.1	19	1	US-08-714-991-14	Sequence 14, Appl
	25	14.8	1.1	19	3	US-09-032-365A-26	Sequence 26, Appl
c	26	14.8	1.1	20	1	US-08-623-891-3	Sequence 3, Appli
c	27	14.8	1.1	20	3	US-09-286-904-42	Sequence 42, Appl
	28	14.8	1.1	20	4	US-09-742-703-11	Sequence 11, Appl
c	29	14.8	1.1	20	4	US-09-340-861-3	Sequence 3, Appli
c	30	14.8	1.1	20	4	US-09-634-262-3	Sequence 3, Appli
c	31	14.8	1.1	20	4	US-09-640-101-42	Sequence 42, Appl
c	32	14.4	1.1	17	4	US-09-359-921-27	Sequence 27, Appl
c	33	14.4	1.1	18	3	US-09-178-115-113	Sequence 113, App
c	34	14.4	1.1	18	3	US-09-177-776-113	Sequence 113, App
c	35	14.4	1.1	20	1	US-08-376-362A-8	Sequence 8, Appli
	36	14.4	1.1	20	1	US-08-634-331-3	Sequence 3, Appli
	37	14.4	1.1	20	2	US-08-450-905B-134	Sequence 134, App
	38	14.4	1.1	20	3	US-07-982-759F-134	Sequence 134, App
c	39	14.4	1.1	20	3	US-09-280-805-48	Sequence 48, Appl
	40	14.4	1.1	20	3	US-09-150-460B-2	Sequence 2, Appli
c	41	14.4	1.1	20	3	US-09-228-942-7	Sequence 7, Appli
	42	14.4	1.1	20	4	US-09-517-467B-240	Sequence 240, App
	43	14.2	1.0	19	3	US-08-246-489-7	Sequence 7, Appli
	44	14.2	1.0	20	1	US-08-033-081B-18	Sequence 18, Appl
	45	14.2	1.0	20	2	US-08-117-952-417	Sequence 417, App

ALIGNMENTS

RESULT 1
US-09-244-794A-29
; Sequence 29, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-244-794A-29

Query Match 1.2%; Score 16.4; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 679 GTGGTATTTGGGAGCCAG 696
||||||||||| |||||||
Db 1 GTGGTATTTGTGAGCCAG 18

RESULT 2
US-09-007-005-29
; Sequence 29, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963

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;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-007-005-29

  Query Match             1.2%;  Score 16.4;  DB 3;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 3
US-09-247-190-29
; Sequence 29, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
;  APPLICANT: Szostak, Jack W.
;  APPLICANT: Roberts, Richard W.
;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350005
;  CURRENT APPLICATION NUMBER: US/09/247,190
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-21
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 09/007,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-247-190-29

  Query Match             1.2%;  Score 16.4;  DB 3;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 4
US-09-244-796-29
; Sequence 29, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
;  APPLICANT: Szostak, Jack W.
;  APPLICANT: Roberts, Richard W.
;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350007
;  CURRENT APPLICATION NUMBER: US/09/244,796
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 09/007,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-244-796-29

  Query Match             1.2%;  Score 16.4;  DB 3;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 5
US-09-238-710-29
; Sequence 29, Application US/09238710A
; Patent No. 6518018
; GENERAL INFORMATION:
;  APPLICANT: Szostak, Jack W.
;  APPLICANT: Roberts, Richard W.
;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350004
;  CURRENT APPLICATION NUMBER: US/09/238,710A
;  CURRENT FILING DATE: 1999-01-28
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 09/007,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-238-710-29

  Query Match             1.2%;  Score 16.4;  DB 4;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 6
US-09-136-959A-6
; Sequence 6, Application US/09136959A
; Patent No. 6248522
; GENERAL INFORMATION:
;  APPLICANT: HABERHAUSEN, Gerd
;  APPLICANT:  JOGER, Stephan
;  APPLICANT:  SOBEK, Harald
;  TITLE OF INVENTION: REDUCTION OF CROSS-CONTAMINATIONS IN NUCLEIC ACID
;  TITLE OF INVENTION:  AMPLIFICATIONS
;  FILE REFERENCE: 1614-8065
;  CURRENT APPLICATION NUMBER: US/09/136,959A
;  CURRENT FILING DATE:  1998-08-20
;  PRIOR APPLICATION NUMBER: DE 197 36 062.9
;  PRIOR FILING DATE: 1997-08-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
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;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-136-959A-6

  Query Match             1.2%;  Score 15.8;  DB 3;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.8e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 7
US-09-556-031-2/c
; Sequence 2, Application US/09556031
; Patent No. 6350868
; GENERAL INFORMATION:
;  APPLICANT:  Weston, Brent W.
;  APPLICANT:  Hiller, Kara B.
;  TITLE OF INVENTION:  Antisense Fucosyltransferase Sequences and Methods of
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE:  Weston and Hiller
;  CURRENT APPLICATION NUMBER: US/09/556,031
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER:  60/131,068
;  PRIOR FILING DATE:  1999-04-26
;  NUMBER OF SEQ ID NOS:  24
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:antisense
;   OTHER INFORMATION: oligonucleotide
US-09-556-031-2

  Query Match             1.2%;  Score 15.8;  DB 4;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.8e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1322 CTTTTGTAGATCTTGTGTT 1340
              |||||||||||||||  |||
Db         19 CTTTTGTAGATCTTCAGTT 1


RESULT 8
US-09-702-246-25/c
; Sequence 25, Application US/09702246
; Patent No. 6383809
; GENERAL INFORMATION:
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF CYTOHESIN-1 EXPRESSION
;  FILE REFERENCE:  RTS-0195
;  CURRENT APPLICATION NUMBER: US/09/702,246
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  89
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-246-25

  Query Match             1.2%;  Score 15.8;  DB 4;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.8e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              |||||||||||||||  ||
Db         20 ACCTGCCGGAGGAGCTCCT 2


RESULT 9
US-09-322-624-19
; Sequence 19, Application US/09322624
; Patent No. 6548734
; GENERAL INFORMATION:
;  APPLICANT: Glimcher, L et al.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MODULATION OF
;  TITLE OF INVENTION: CARTILAGE GROWTH BY MODULATION OF NFATp ACTIVITY
;  FILE REFERENCE: HUI-035CP
;  CURRENT APPLICATION NUMBER: US/09/322,624
;  CURRENT FILING DATE: 1999-05-28
;  EARLIER APPLICATION NUMBER: USSN 09/087,139
;  EARLIER FILING DATE: 1998-05-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: synthetic construct
US-09-322-624-19

  Query Match             1.2%;  Score 15.8;  DB 4;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.8e+05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        934 CTGGAGAAGAGGTGTGAGC 952
              |||||||||||| | |||||
Db          1 CTGGAGAAGAGCTATGAGC 19


RESULT 10
US-09-422-978-11451/c
; Sequence 11451, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11451
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-6707 for SEQ 3586, in compl
US-09-422-978-11451

  Query Match             1.1%;  Score 15.4;  DB 4;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.3e+05;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        225 TCCTCAGCCTCAGGCAT 241
              |||||| ||||||||||
Db         17 TCCTCATCCTCAGGCAT 1
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RESULT 11
US-07-977-284A-89/c
; Sequence 89, Application US/07977284A
; Patent No. 5558988
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Ala-Kokko, Leena
;    APPLICANT:  Williams, Charlene J.
;    APPLICANT:  Ritvaniemi, Pertti
;    APPLICANT:  Baldwin, Clinton
;    APPLICANT:  Hopkinson, Ian
;    APPLICANT:  Ahmad, Nilofer Nina
;    TITLE OF INVENTION:  METHODS OF DETECTING A GENETIC
;    TITLE OF INVENTION:  PREDISPOSITION FOR OSTEOARTHRITIS
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/977,284A
;      FILING DATE:  13-NOV-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-0697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-07-977-284A-89

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCTG 301
              |||||||||||||  || | |
Db         20 GGAAGCAGCAGCAGTGACAG 1


RESULT 12
US-08-410-540-8/c
; Sequence 8, Application US/08410540
; Patent No. 5807678
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Walter L.
;    APPLICANT:  Lin, Dong
;    APPLICANT:  Strauss III, Jerome F.
;    TITLE OF INVENTION:  IDENTIFICATION OF GENE MUTATIONS
;    TITLE OF INVENTION:  ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,540
;      FILING DATE:  23-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard L.
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  UCAL-238/00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415 853 5070
;      TELEFAX:  415 857 0663
;      TELEX:  380816COOLEYPA
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-410-540-8

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 TGCTGGCAGGCATGCACACA 567
              ||||||| ||||||  ||||
Db         20 TGCTGGCTGGCATGGCCACA 1


RESULT 13
US-08-256-426B-89/c
; Sequence 89, Application US/08256426B
; Patent No. 5948611
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Ala-Kokko, Leena
;    APPLICANT:  Williams, Charlene J.
;    APPLICANT:  Ritvaniemi, Pertti
;    APPLICANT:  Baldwin, Clinton
;    APPLICANT:  Hopkinson, Ian
;    APPLICANT:  Ahmad, Nilofer Nina
;    TITLE OF INVENTION:  Methods of Detecting A Genetic
;    NUMBER OF SEQUENCES:  293
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/256,426B
;      FILING DATE:  03-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  PCT/US93/10964
;      FILING DATE:  12-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,284
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mark DeLuca
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-1082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-08-256-426B-89

  Query Match             1.1%;  Score 15.2;  DB 2;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCTG 301
              |||||||||||| || | |
Db         20 GGAAGCAGCAGCAGTGACAG 1


RESULT 14
US-09-661-753-55
; Sequence 55, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT: Susan F. Murray
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
;  FILE REFERENCE: ISPH-0498
;  CURRENT APPLICATION NUMBER: US/09/661,753
;  CURRENT FILING DATE: 2000-09-14
;  EARLIER APPLICATION NUMBER: 60/154,546
;  EARLIER FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-55

  Query Match             1.1%;  Score 15.2;  DB 4;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        621 CAGGGACCAGCTCCAGGAGC 640
              | |||||||| | |||||||
Db          1 CCGGGACCAGATGCAGGAGC 20


RESULT 15
US-09-470-443-33
; Sequence 33, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT: Minna, John D.
;  APPLICANT: Latif, Farida
;  APPLICANT: Wei, Ming-Hui
;  APPLICANT: Sekido, Yoshitaka
;  APPLICANT: Gao, Boning
;  APPLICANT: Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/09/470,443
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/114,359
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-470-443-33

  Query Match             1.1%;  Score 15.2;  DB 4;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+05;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CTGGTGATAGTCACAGTGGC 354
              |||||||| |||||||  ||
Db          1 CTGGTGATGGTCACAGGAGC 20


Search completed: September  7, 2003, 20:05:23
Job time : 98.5886 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 20:02:22 ; Search time 366.485 Seconds
(without alignments)
9980.603 Million cell updates/sec

Title: US-09-904-568-3
Perfect score: 1355
Sequence: 1 gggcaggcagttgaggtgga.....gtgtttcaggcagggcccgg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1495040

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	1.5	20	21	AAC67508	Alzheimer's diseas
	2	16.4	1.2	18	19	AAV48107	Beta-globin fusion
	3	16.4	1.2	18	21	AAC67511	Alzheimer's diseas
	4	16.4	1.2	18	21	AAA94334	Human beta-globin
	5	15.8	1.2	20	20	AAX22417	EP-897990 Seq ID 6
c	6	15.8	1.2	20	21	AAC68751	Human FUT3 antisen
	7	15.8	1.2	20	21	AAZ45870	PCR primer R1570RA
	8	15.8	1.2	20	21	AAZ60204	PCR primer F1570RA
	9	15.8	1.2	20	21	AAZ56049	PCR primer for bet
	10	15.8	1.2	20	22	AAH25407	Detection probe fo
c	11	15.8	1.2	20	24	ABS73911	Human cytohesin-1
	12	15.8	1.2	20	24	ABN83653	Human immunodefici
c	13	15.8	1.2	20	24	ABQ66447	Human cytohesin-1
	14	15.8	1.2	20	24	ABK51604	Human immunodefici
c	15	15.8	1.2	20	24	ABA04617	MOL2 forward PCR p
c	16	15.4	1.1	18	24	ABK85826	Myotonic dystrophy
	17	15.4	1.1	18	24	AAI71035	Human tumour suppr
	18	15.4	1.1	20	16	AAT03278	Mycobacterium tube
c	19	15.4	1.1	20	21	AAZ77095	Human biallelic ma
c	20	15.2	1.1	20	15	AAQ65816	Type II procollage
c	21	15.2	1.1	20	17	AAT39478	Steroidogenesis ac
	22	15.2	1.1	20	20	AAZ04965	PCR primer used to
c	23	15.2	1.1	20	20	AAX94626	PCR primer used to
c	24	15.2	1.1	20	20	AAX92281	PCR primer used to
	25	15.2	1.1	20	20	AAX33259	PEBP2 alpha A gene
	26	15.2	1.1	20	24	ABS74296	Human calcium chan
	27	15.2	1.1	20	24	ABS74306	Human calcium chan
	28	15.2	1.1	20	24	ABS76637	Novel metalloprote
c	29	15.2	1.1	20	24	ABS67685	Casein kinase-2 an
	30	15.2	1.1	20	24	ABK69390	Chimeric phosphoro
	31	15	1.1	15	20	AAX31672	Tag sequence of a
	32	15	1.1	15	24	ABK32626	Human pancreatic c
c	33	15	1.1	17	24	ABK12664	Rat interleukin 11
c	34	15	1.1	18	22	AAF62379	LSR-leptin interac
c	35	14.8	1.1	18	17	AAX67028	Mouse B7 hairpin r
	36	14.8	1.1	18	25	AAD52710	Psammomys obesus A
	37	14.8	1.1	19	18	AAT96652	Mouse tub gene pri
	38	14.8	1.1	19	21	AAA94645	Mouse tub gene PCR
	39	14.8	1.1	19	21	AAA84761	Cyclin F ribozyme
	40	14.8	1.1	19	22	AAH59923	Cyclin F ribozyme
c	41	14.8	1.1	19	22	AAF91219	Human multi drug r
	42	14.8	1.1	19	22	AAF91221	Human multi drug r
c	43	14.8	1.1	20	14	AAQ52925	Herpes simplex vir
	44	14.8	1.1	20	20	AAZ02840	PCR primer used to
c	45	14.8	1.1	20	21	AAA70403	Plant beta-tubulin

ALIGNMENTS

RESULT 1
AAC67508/c
ID AAC67508 standard; DNA; 20 BP.
XX
AC AAC67508;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #208.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Davis RE;
XX
DR WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease

PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
PS Example 9; Page 51; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In additon, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;

Query Match 1.5%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 CAGCTACGCAAAATCTTAGC 52
||||||||||||||||||||
Db 20 CAGCTACGCAAAATCTTAGC 1

RESULT 2
AAV48107
ID AAV48107 standard; DNA; 18 BP.
XX
AC AAV48107;
XX
DT 27-OCT-1998 (first entry)
XX
DE Beta-globin fusion primer 18.155.
XX
KW In situ translation; RNA-protein fusion; binding reagent; antibody;
KW industrial catalyst; ss; PCR; primer; amplification.
XX
OS Synthetic.
XX
PN WO9831700-A1.
XX
PD 23-JUL-1998.
XX
PF 14-JAN-1998; 98WO-US00807.
XX
PR 06-NOV-1997; 97US-0064491.
PR 21-JAN-1997; 97US-0035963.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Liu R, Roberts RW, Szostak JW;
XX
DR WPI; 1998-414032/35.
XX
PT Selection of specific protein by screening protein-RNA fusions
PT generated in vitro or in situ - useful for, e.g. identifying enzymes
PT and antibodies with altered properties, potentially useful as
PT catalysts or for therapy or diagnosis
XX
PS Disclosure; Page 49; 94pp; English.
XX
CC The primers AAV48107 and AAV48108 were used in the synthesis of a
CC beta-globin fusion construct. This was used in the selection of a
CC specific protein or RNA, by in vitro or in situ translation of candidate
CC RNA molecules to produce RNA-protein fusions, then selecting specific RNA
CC protein fusions. The method is used to select proteins (or DNA encoding
CC them) having altered properties, e.g. for identification of new binding
CC reagents, to identify improved human antibodies or new enzymes. These
CC proteins are potentially useful in diagnosis and therapy, or as
CC industrial catalysts. The methods allow many rounds of selection and
CC amplification to be performed, resulting in enrichment of even very rare
CC molecules and allowing isolation of proteins that bind specifically to
CC almost any compound or catalyse almost any reaction.
XX
SQ Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;

Query Match 1.2%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 679 GTGGTATTTGGGAGCCAG 696
||||||||||.|||||||
Db 1 GTGGTATTTGTGAGCCAG 18

RESULT 3
AAC67511
ID AAC67511 standard; DNA; 18 BP.
XX
AC AAC67511;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #211.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Davis RE;
XX
DR WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
PS Example 9; Page 51; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In additon, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 18 BP; 7 A; 7 C; 3 G; 1 T; 0 other;

Query Match 1.2%; Score 16.4; DB 21; Length 18;
Best Local Similarity 94.4%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 23 AAACCAAACCCAGCTACG 40
|||||| ||||||||||
Db 1 AAACCAGACCCAGCTACG 18

RESULT 4
AAA94334
ID AAA94334 standard; DNA; 18 BP.
XX

```
AC   AAA94334;
XX
DT   11-JAN-2001  (first entry)
XX
DE   Human beta-globin mRNA reverse transcription primer 18.155.
XX
KW   Human; beta-globin; RNA-protein fusion; protein library;
KW   protein isolation; gene cloning; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US02589.
XX
PR   09-FEB-1999;   99US-0247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions -
XX
PS   Disclosure; Page 55; 121pp; English.
XX
CC   The present sequence is a primer which was used to generate beta-globin
CC   cDNA from mRNA by reverse transcription. The cDNA was used in a method
CC   for generating beta-globin RNA-protein fusions. RNA-protein fusions
CC   comprise a protein covalently linked to the 3' end of its own mRNA. The
CC   fusions are made by synthesis and in vitro or in situ translation of an
CC   mRNA molecule with a peptide acceptor attached to its 3' end. The
CC   RNA-protein fusions are incubated under high salt conditions to produce
CC   a protein library. This method is useful for improving or altering
CC   existing proteins, as well as for isolating new proteins and nucleic
CC   acid or small molecule targets. It may also be used to improve human or
CC   humanised single-chain antibodies for the treatment of a number of
CC   diseases. The method is useful for the isolation of proteins with
CC   specific binding properties, for screening cDNA libraries and cloning
CC   new genes on the basis of protein-protein interactions. Unlike prior
CC   art, the new method does not rely on maintaining the integrity of an
CC   mRNA:ribosome:nascent chain ternary complex, which is very fragile and
CC   is therefore of limited use. The method does not rely on topological
CC   links between the protein and the nucleic acid so that the information
CC   of the protein is retained and can be recovered in readable, nucleic
CC   acid form.
XX
SQ   Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.4;  DB 21;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 7.7e+05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              ||||||||||  |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 5
AAX22417
ID   AAX22417 standard; DNA; 20 BP.
XX
AC   AAX22417;
XX
DT   20-MAR-2003  (updated).
DT   19-MAY-1999  (first entry)
XX
DE   EP-897990 Seq ID 6.
XX
KW   Cross-contamination; amplification; N-lauroylsarcosine; inhibition;
KW   reactivation; uracil-N-glycosylase; UNG; false negative; primer; ss.
XX
OS   Synthetic.
XX
PN   EP897990-A2.
XX
PD   24-FEB-1999.
XX
PF   18-AUG-1998;   98EP-0115491.
XX
PR   20-AUG-1997;   97DE-1036062.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Haberhausen G,  Jaeger S,  Sobek H;
XX
DR   WPI; 1999-134649/12.
XX
PT   Prevention of cross-contamination in DNA amplification - using
PT   nucleic-acid-degrading enzyme and reagent that inhibits reactivation
PT   of inactivated enzyme
XX
PS   Example 2; Page 8; 17pp; German.
XX
CC   This sequence is used to describe a method for reducing
CC   cross-contamination during the amplification of nucleic acids in a
CC   sample. The method involves (i) treating the sample with an enzyme
CC   that degrades nucleic acids from other amplification reactions; (ii)
CC   inactivating the enzyme; and (iii) amplifying the nucleic acids in the
CC   sample in the presence of a reagent that inhibits reactivation of the
CC   enzyme. N-lauroylsarcosine is used to inhibit reactivation of
CC   uracil-N-glycosylase (UNG). The new method prevents cross-contamination
CC   from amplification products containing artificially introduced dUTP
CC   units by using UNG and inhibiting reactivation of the UNG as above
CC   eliminates false negatives.
CC   (Updated on 20-MAR-2003 to correct PA field.)
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 20;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              |||||  ||||||||  ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 6
AAC68751/c
ID   AAC68751 standard; DNA; 20 BP.
XX
AC   AAC68751;
XX
DT   20-FEB-2001  (first entry)
XX
DE   Human FUT3 antisense oligonucleotide SEQ ID NO: 2.
XX
KW   Human; fucosyltransferase; FUT3; FUT6; cancer; antisense oligonucleotide;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200064262-A1.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-US10547.
XX
```

```
PR   26-APR-1999;  99US-0131068.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Weston BW,  Hiller KM;
XX
DR   WPI; 2000-687246/67.
XX
PT   Novel antisense human fucosyltransferase sequences useful for treating
PT   cancer including breast, lung, gastric, renal and uterine cancer -
XX
PS   Claim 6; Page 32; 53pp; English.
XX
CC   The present invention provides antisense oligonucleotides to the human
CC   fucosyltransferase coding sequences, particularly FUT3 and FUT6. These
CC   antisense sequences can be used in the treatment of cancer, especially
CC   colon, pancreatic, ovarian, gastric, breast, lung, hepatocellular,
CC   prostate, bladder, renal cell and uterine cancers. In additon, they can
CC   also be used in the treatment of animals such as dogs, cats and horses.
XX
SQ   Sequence 20 BP; 11 A; 3 C; 3 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 21;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1322 CTTTTGTAGATCTTGTGTT 1340
              ||||||||||||||  |||
Db         19 CTTTTGTAGATCTTCAGTT 1


RESULT 7
AAZ45870
ID   AAZ45870 standard; DNA; 20 BP.
XX
AC   AAZ45870;
XX
DT   25-APR-2000  (first entry)
XX
DE   PCR primer R1570RAP used to amplify a portion of the RAP3 gene.
XX
KW   RAP3; regeneration association protein 3; liver regeneration;
KW   liver proliferation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200003013-A2.
XX
PD   20-JAN-2000.
XX
PF   12-JUL-1999;  99WO-EP04938.
XX
PR   10-JUL-1998;  98EP-0202336.
XX
PA   (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
PI   Chamuleau RAFM,  Groenink M,  Van Der Vliet HN,  Leegwater ACJ;
XX
DR   WPI; 2000-147615/13.
XX
PT   Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT   regeneration and/or cell proliferation -
XX
PS   Disclosure; Page 3; 42pp; English.
XX
CC   AAZ45854-71 represent PCR primers, derived from the human RAP3 cDNA
CC   sequence. The RAP3 (regeneration association protein 3) gene is
CC   involved in regeneration processes of the liver. The RAP3 gene was
CC   found to be upregulated 6 hours after partial hepatectomy, after
CC   which it is downregulated. The PCR primers are useful for detecting
CC   nucleotide sequences in a source material. The RAP3 cDNA sequence
CC   is useful as a  marker of liver proliferation. The RAP3 protein is
CC   useful for the diagnosis of liver regeneration and liver cell
CC   proliferation. RAP3 antibodies, PCR primers and probes are useful
CC   for detecting the occurrence of liver cell proliferation in a patient.
CC   The RAP3 protein is also is useful for enhancing the growth of
CC   regeneration of liver tissue comprising treating the liver tissue
CC   such as extracorporeal or intracorporeal.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 21;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        551 TGGCAGGCATGCACACACT 569
              ||||||| ||| |||||||
Db          1 TGGCAGGGATGTACACACT 19


RESULT 8
AAZ60204
ID   AAZ60204 standard; cDNA; 20 BP.
XX
AC   AAZ60204;
XX
DT   25-APR-2000  (first entry)
XX
DE   PCR primer F1570RAP for RAP3 identification or amplification.
XX
KW   RAP3; rat; liver regeneration; hepatic cell proliferation; liver biopsy;
KW   liver transplant; bioartificial liver; PCR primer; ss.
XX
OS   Rattus sp.
XX
PN   EP976824-A1.
XX
PD   02-FEB-2000.
XX
PF   10-JUL-1998;  98EP-0202336.
XX
PR   10-JUL-1998;  98EP-0202336.
XX
PA   (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
PI   Chamuleau RAFM,  Groenink M,  Van der Vliet HN,  Leegwater ACJ;
XX
DR   WPI; 2000-147615/13.
XX
PT   Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT   regeneration and/or cell proliferation -
XX
PS   Claim 15; Page 3; 31pp; English.
XX
CC   This sequence represents a PCR primer which is based on the rat RAP3
CC   gene. The RAP3 gene and rap3 protein are involved in the regeneration
CC   processes of the liver, and the RAP3 gene is expressed specifically in
CC   the liver. The RAP3 gene is useful for designing PCR primers (such as the
CC   present sequence) and probes for detecting nucleotide sequences in a
CC   source material and as a marker of liver proliferation. The rap3 protein
CC   is useful for the diagnosis of liver regeneration and/or liver cell
CC   proliferation. Anti-rap3 antibodies, PCR primers and nucleotide sequences
CC   which act as probes are useful for detecting the occurrence of liver cell
CC   proliferation in a patient. Single stranded oligonucleotides that are
CC   complementary to RAP3 can be used as probes to detect the amount of mRNA
CC   transcribed from RAP3 present in a sample such as a liver biopsy, plasma
CC   or serum of a tissue or body fluid in comparison to a reference sample.
CC   The probes can also be used for screening a liver cDNA or genomic
CC   library. The rap3 protein is useful for enhancing the growth or
CC   regeneration of liver tissue. The methods of the invention can be used to
CC   establish the efficacy of therapeutic agents stimulating liver
CC   regeneration and for patients who have undergone liver transplantation
CC   and for monitoring patients treated with a bioartificial liver.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;
```

```
  Query Match             1.2%;  Score 15.8;  DB 21;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        551 TGGCAGGCATGCACACACT 569
              ||||||| ||| |||||||
Db          1 TGGCAGGGATGTACACACT 19


RESULT 9
AAZ56049
ID   AAZ56049 standard; DNA; 20 BP.
XX
AC   AAZ56049;
XX
DT   23-MAR-2000  (first entry)
XX
DE   PCR primer for beta-actin.
XX
KW   Nuclear factor of activated T cells; NFATp; bone fracture; osteoporosis;
KW   calcineurin interaction region; cartilage cell differentiation;
KW   endochondral ossification; chondrosarcoma; rheumatoid arthritis;
KW   osteoarthritis; osteosarcoma; fibrous sarcoma; chondroma; enchondroma;
KW   PCR primer; beta-actin; ss.
XX
OS   Mus sp.
XX
PN   WO9961908-A1.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US11941.
XX
PR   28-MAY-1998;   98US-0087139.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Glimcher LH,  Ranger AM;
XX
DR   WPI; 2000-086734/07.
XX
PT   Modulating growth or differentiation of cartilage cells useful for
PT   treating chondrosarcoma, osteochondroma and arthritis in mammals -
XX
PS   Example 6; Page 57; 90pp; English.
XX
CC   PCR primers AAZ56049-Z56050 are used to amplify beta-actin from wild
CC   type and NFATp-/- cartilage cultures. The primers are used in the
CC   identification of the role that NFATp plays in cartilage cell growth and
CC   differentiation. The modulation of growth or differentiation of
CC   cartilage can be carried out through contacting cells deficient in the
CC   NFAT family genes, with a  test compound. Modulating growth or
CC   differentiation of cartilage cells can achieved by contacting the cells
CC   with a modulator of NFATp activity, where the modulator comprises a
CC   peptidic compound derived from the calcineurin interacting region of
CC   NFATp. The methods of the invention are useful for modulating the growth
CC   or differentiation of cartilage cells and endochondral ossification
CC   useful for repairing bone defects and fractures in mammals including
CC   humans, monkeys, dogs, cats, mice etc. The compound that modulates
CC   cartilage cell growth and differentiation is useful for diagnosing
CC   disorders such as chondrosarcoma, osteochondroma, chondromyxoid fibroma,
CC   chondroma, enchondroma, chondroblastoma, osteoblastoma, fibrous
CC   dysplasia, ossifying fibroma, osteosarcoma or osteocartilaginous
CC   exostosis, which are associated with a change (elevated, reduced or
CC   mutated) in the expression of NFATp in cartilage cell. NFATp inhibitory
CC   compounds are useful for treating disorders such as rheumatoid arthritis,
CC   osteoarthritis and osteoporosis associated with cartilage degradation.
XX
SQ   Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 21;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        934 CTGGAGAAGAGGTGTGAGC 952
              |||||||||||  | |||||
Db          1 CTGGAGAAGAGCTATGAGC 19


RESULT 10
AAH25407
ID   AAH25407 standard; DNA; 20 BP.
XX
AC   AAH25407;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Detection probe for a HIV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS   Human immunodeficiency virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11459.
XX
PR   17-NOV-1999;   99EP-0122853.
PR   12-MAY-2000; 2000EP-0110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA
PT   or RNA in automated processes -
XX
PS   Example 7; Page 96; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between
CC   5-500 nm. The composition is useful for the purification of nucleic
CC   acids. The composition can be used to process large quantities of
CC   nucleic acid samples, because it does not involve the particles being
CC   centrifuged or the fluids being drawn through glass fiber filters.
CC   The present sequence represents a probe for a HIV DNA fragment. The
CC   DNA fragment can be purified using the method of the invention.
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 22;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 11
ABS73911/c
ID   ABS73911 standard; DNA; 20 BP.
XX
AC   ABS73911;
XX
DT   06-DEC-2002  (first entry)
XX
```

```
DE   Human cytohesin-1 coding region antisense oligonucleotide, ISIS#111004.
XX
KW   Human; antisense; cytohesin-1; guanine nucleotide exchange protein;
KW   ARF; ADP ribosylation factor; inflammation; antiinflammatory; tumour;
KW   cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200268584-A2.
XX
PD   06-SEP-2002.
XX
PF   30-OCT-2001; 2001WO-US47583.
XX
PR   22-FEB-2001; 2001US-0791243.
XX
PA   (ISIS-) ISIS PHARM INC.
PA   (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI   Bennett CF,  Rothlein R,  Kishimoto TK,  Cowsert LM;
XX
DR   WPI; 2002-723198/78.
XX
PT   New antisense oligonucleotide encoding human cytohesin-1, useful for
PT   preventing or treating a disease or condition associated with
PT   cytohesin-1 expression e.g. tumor or inflammation -
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to a new antisense compound, comprising 8-30
CC   nucleobases targeted to a nucleic acid molecule encoding human
CC   cytohesin-1, specifically hybridises with, and inhibits the expression
CC   of, human cytohesin-1, a guanine nucleotide exchange protein for ARF
CC   (ADP ribosylation factor). The antisense compound may be used in a
CC   pharmaceutical composition for inhibiting the expression of
CC   cytohesin-1 in human cells or tissues, and in treating a disease or
CC   condition associated with cytohesin-1 by administering to the human the
CC   antisense compound e.g. tumour or inflammation. The antisense
CC   compound is also useful for diagnostics, therapeutics, prophylaxis and
CC   as research reagents and kits. The present sequence is an antisense
CC   oligonucleotide targeting human cytohesin-1.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 24;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              ||||||||||||||||  ||
Db         20 ACCTGCCGGAGGAGCTCCT 2


RESULT 12
ABN83653
ID   ABN83653 standard; DNA; 20 BP.
XX
AC   ABN83653;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human immunodeficiency virus capture probe.
XX
KW   Nucleic acid detection; infection; subtilisin; esperase; diagnosis;
KW   HIV; probe; ss.
XX
OS   Human immunodeficiency virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag= a
FT                    /mod_base= OTHER
FT                    /note= "Ruthenium-tris(bipyridyl) label"
XX
PN   EP1201752-A1.
XX
PD   02-MAY-2002.
XX
PF   31-OCT-2000; 2000EP-0123728.
XX
PR   31-OCT-2000; 2000EP-0123728.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Schmuck R,  Staepels J,  Meier T,  Wehnes U,  Russmann E;
XX
DR   WPI; 2002-396142/43.
XX
PT   Use of Bacillus lentus subtilisin 147 to analyze one or more target
PT   non-proteinaceous components from a mixture of non-proteinaceous and
PT   proteinaceous components derived from a biological sample useful e.g.
PT   diagnostically -
XX
PS   Example; Page 24; 36pp; English.
XX
CC   The present sequence is a human immunodeficiency virus (HIV)
CC   capture probe, labeled with ruthenium-tris(bipyridyl) label.  The
CC   probe was used with HIV PCR primers (see ABN83651-52) in an example
CC   from the invention for the amplification and detection of HIV RNA
CC   in a plasma sample.  The invention provides a method for the
CC   analysis of non-proteinaceous components, especially DNA and/or
CC   RNA, in a mixture of proteinaceous and non-proteinaceous components
CC   in a biological sample.  The sample is incubated with protease
CC   subtilisin 147 (see ABB76400) of Bacillus lentus variant 147
CC   (NCIB 10147), and the target DNA or RNA is then amplified by PCR
CC   and determined or detected.  In the present example, the
CC   ruthenium-tris(bipyridyl)-labeled capture probe provided a
CC   sensitive nonisotopic approach to detection based on
CC   electrochemiluminescence following specific hybridisation to
CC   biotinylated denatured HIV amplicons.  The method is useful in
CC   environmental, food and medical analysis, e.g. to detect viral
CC   infection, and in molecular biological research, and can be
CC   performed using a high throughput format.
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 24;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+06;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 13
ABQ66447/c
ID   ABQ66447 standard; DNA; 20 BP.
XX
AC   ABQ66447;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human cytohesin-1 mRNA levels inhibitor #16.
XX
KW   Cytohesin-1; CT1; inhibit; cytostatic; antiinflammatory; cytostatic;
KW   anti-infective; antisense gene therapy; infection; inflammation; tumour;
KW   human; ss; inhibitor.
XX
OS   Synthetic.
XX
PN   US6383809-B1.
XX
PD   07-MAY-2002.
XX
PF   30-OCT-2000; 2000US-0702246.
```

XX
PR 30-OCT-2000; 2000US-0702246.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2002-478385/51.
XX
PT New antisense compounds directed against human cytohesin-1, useful for
PT treating and preventing infection, inflammation and tumors -
XX
PS Claim 14; Column 41; 40pp; English.
XX
CC The invention relates to a novel antisense compound of 16-30 nucleotides
CC targeted to any of 71 specified regions of the sequence that encodes
CC human cytohesin-1 (CT1), where the compound hybridises and inhibits
CC expression of human CT1. The compound of the invention has
CC antiinflammatory, cytostatic, and anti-infective activity. The
CC antisense compounds may have a use in antisense gene therapy. The
CC antisense compounds are useful for treating or preventing disorders
CC associated with expression of human CT1, e.g. infections, inflammation
CC and tumours, and as research and diagnostic reagents. Sequences
CC ABQ66432-ABQ66511 represent chimeric phosphorothioate oligonucleotides,
CC with 2'-MOE wings and a deoxy gap. The claimed sequences inhibit
CC production of cytohesin-1 mRNA.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 521 ACCTGCCGGAGGAGCAGCT 539
||||||||||||||| ||
Db 20 ACCTGCCGGAGGAGCTCCT 2

RESULT 14
ABK51604
ID ABK51604 standard; DNA; 20 BP.
XX
AC ABK51604;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus (HIV) protease, probe.
XX
KW Subtilisin 147; medical analysis; environmental analysis;
KW food analysis; diagnostic; virus infection; probe; ss;
KW human immunodeficiency virus; HIV; protease.
XX
OS Human immunodeficiency virus.
XX
PN EP1201753-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001EP-0125322.
XX
PR 31-OCT-2000; 2000EP-0123728.
PR 15-MAR-2001; 2001EP-0106308.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Russmann E, Schmuck R, Meier T, Staepels J, Wehnes U;
XX
DR WPI; 2002-428566/46.
XX
PT Use of Bacillus lentus subtilisin 147 to analyse a target
PT non-proteinaceous component from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically to detect viruses -
XX
PS Example 2; Page 26; 38pp; English.
XX
CC The invention describes a target non-proteinaceous component is
CC analysed from a mixture of non-proteinaceous and proteinaceous components
CC derived from a biological sample by incubating the mixture with a
CC protease having at least 80 % identity to the known amino acid sequence
CC for subtilisin 147 from Bacillus lentus. The methods are useful for
CC analysis of biological samples e.g. in medical, environmental or food
CC analysis or in molecular biological research. They are especially useful
CC in diagnostics e.g. to detect virus infections. They can be used to
CC enrich a mixture for a target non-proteinaceous component or
CC purify/isolate the component, the component can especially be a nucleic
CC acid, e.g. from a virus/microorganism. The methods can be used to
CC isolate non-proteinaceous components useful as substrates in enzymatic
CC reactions, or (in the case of nucleic acids) for sequencing, as probes
CC etc. They can be used in high throughput formats, enabling analysis of
CC large numbers of samples in a short time. Kits for undertaking the
CC methods, comprising the preferred polypeptide, optionally a material
CC with an affinity to nucleic acids (especially preferred materials as
CC above) and/or optionally lysis, washing and elution buffers are provided.
CC This sequence represents a probe used to detect DNA sequences encoding
CC Human immunodeficiency virus proteases.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 274 ATCAAAGAGGAAGCAGCAG 292
||||| |||||||| ||||
Db 1 ATCAATGAGGAAGCTGCAG 19

RESULT 15
ABA04617/c
ID ABA04617 standard; DNA; 20 BP.
XX
AC ABA04617;
XX
DT 21-FEB-2002 (first entry)
XX
DE MOL2 forward PCR primer.
XX
KW MOL; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
KW cell signal processing; metabolic disorder; diabetes; cancer;
KW neurodegenerative disorder; immune disorder; cardiac disorder;
KW lung disease; autoimmune disease; developmental disorder; antidiabetic;
KW Cytostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
KW Gene therapy; Vaccine; antiinflammatory; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200181578-A2.
XX
PD 01-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US13578.
XX
PR 26-APR-2000; 2000US-200158P.
PR 28-APR-2000; 2000US-200613P.
PR 28-APR-2000; 2000US-200780P.
PR 01-MAY-2000; 2000US-201006P.
PR 01-MAY-2000; 2000US-201007P.
PR 01-MAY-2000; 2000US-201236P.
PR 01-MAY-2000; 2000US-201238P.
PR 02-MAY-2000; 2000US-201186P.
PR 03-MAY-2000; 2000US-201474P.
PR 03-MAY-2000; 2000US-201508P.
PR 25-JUL-2000; 2000US-220591P.
PR 15-SEP-2000; 2000US-232678P.

PR 22-JAN-2001; 2001US-263217P.
PR 30-JAN-2001; 2001US-265160P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Fernandes ER, Gerlach V, Shimkets RA, Malyankar UM;
PI Boldog FL, Zerhusen BD, Spytek KA, Majumder K, Tchernev VT;
PI Padigaru M, Patturajan M, Burgess CE, Gangolli EA, Smithson G;
PI Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
PI Alsobrook JP;
XX
DR WPI; 2002-049278/06.
XX
PT Novel G-protein coupled receptor-related polypeptides and
PT polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT atherosclerosis, disorders related to cell signal processing and for
PT identifying modulators -
XX
PS Example 1; Page 156; 227pp; English.
XX
CC The present invention relates to novel G-coupled protein-receptor related
CC proteins and coding sequences (MOLX, where X is a number from 1 to 10,
CC ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
CC sequences are useful for treating or preventing a MOLX-associated
CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC cell signal processing and metabolic pathway modulation, diabetes and
CC cancer. Additionally, MOLX proteins and coding sequences are useful for
CC preventing and treating a variety of disorders including metabolic
CC disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC obesity, infectious disease, anorexia, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC and wasting disorders associated with chronic diseases and cancers,
CC cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC scleroderma, autoimmune diseases, developmental disorders and neural tube
CC defects. The present sequence is a PCR primer, which was used to
CC illustrate the invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 641 TCTGCATCCCCCAAGACCT 659
||||||||| ||||||| |
Db 19 TCTGCATCCACCAAGACAT 1

Search completed: September 7, 2003, 22:34:46
Job time : 367.485 secs